

The Ghost of L51: Genetics, Languages, and the Black Hole of the Atlantic Bronze Age



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Desde el rincón de la Izquierda

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Imagen de portada: Marcos J. Correa, Variación y deformación de sobre la obra de Olga Rozanova Pintura en color (variación no objetiva). 1917.
Museo Estatal Ruso, San Petersburgo



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The Ghost of L51: Genetics, Languages, and the Black Hole of the Atlantic Bronze Age

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Abstract

This article examines the relationship between the distribution of Y-chromosomal haplogroup R1b in Western Europe, the non-Indo-European languages historically documented in the Mediterranean basin, and the critical absence of ancient DNA data from the Atlantic seaboard during the third millennium BC. Starting from the Basque paradox — a population with 87% R1b that speaks a non-Indo-European language — the analysis extends to the Etruscans (75% R1b, non-IE language), the Iberians, and the Aquitanians, all of whom are linked to the Urnfield culture. It is demonstrated that the conventional equation “non-Indo-European = pre-Indo-European” constitutes a logical error that has distorted the interpretation of genetic and linguistic evidence for decades. Finally,



it is documented that the R1b-L51 subclade — ancestor of all Western European R1b — has never been found in the Pontic steppe, and that the Atlantic finisterre, where the highest R1b frequencies on the planet are recorded today, entirely lacks ancient DNA samples from the Bronze Age. This double absence — L51 in the steppe, ancient DNA in the Atlantic — opens the possibility that the conventionally assumed direction of R1b's journey (east → west) is an assumption unsupported by empirical data.

Keywords: R1b, L51, Z2103, Atlantic Bronze Age, non-Indo-European languages, Urnfield culture, haplogroup H, Pontic steppe, Basque paradox, population genetics.

I. The Labyrinths of the Atlantic Bronze Age and the Question of Their Makers

This article was born from a lateral question. While studying the stone-carved labyrinths of the Iberian northwest — the Mogor labyrinth (Marín, Pontevedra), Os Campiños (Poio, Pontevedra), those of Peña Fadiel (Filiel, Lucillo, León) — we stumbled upon a paradox we had not anticipated. The Atlantic Bronze Age labyrinths, dated between the second and first millennia BC, constitute one of the most sophisticated symbolic manifestations of prehistoric Europe. The classical seven-circuit labyrinth, present from Galicia to Scandinavia, from Cornwall to the central Mediterranean, obeys a mathematically rigorous constructive logic that we have described elsewhere (Correa López 2026). It is neither improvised nor accidental: it is the product of a technical tradition shared by



peoples who inhabited the Atlantic coasts during the Bronze Age.

The question we asked was simple: who were these peoples? What do we know about the makers of Mogor?

The answer was disconcerting: almost nothing. The Atlantic Bronze Age is one of the great paradoxes of European archaeology. We know its material culture: the petroglyphs, the hoards of axes and swords, the tin trade routes. We know its symbolism: the deer, the spirals, the labyrinths. But of the makers themselves — of their bodies, their genetics — we know extraordinarily little.

Atlantic Bronze Age burials are scarce and generally poorly preserved. The dominant funerary practice along the Atlantic seaboard from the Late Neolithic through the Iron Age does not favour the preservation of skeletal remains. The acidic soils of Galicia, Brittany, and Ireland destroy collagen. And there is a deeper problem: the Atlantic peoples may not have buried their dead in earth at all. The evidence from riverine deposits — weapons, axes, personal ornaments found in rivers, estuaries, and bogs — suggests that the Atlantic Bronze Age communities consigned their dead to water (Ruiz-Gálvez Priego 1995). If the dead were given to the river, there are no bones. If there are no bones, there is no DNA. If there is no DNA, the Atlantic Bronze Age does not exist in the genomic databases.

When we reviewed the ancient population genetics literature, we discovered a gap that confirmed this absence: **there is virtually no ancient DNA from the European Atlantic seaboard between 3000 and 2000 BC.** Not from Galicia. Not from Brittany. Not from Ireland. Not from Atlantic Portugal. The arc from Cape Finisterre to Land's End is, genetically speaking, terra incognita for the third millennium.

What we do know is that the modern populations of this same



Atlantic arc share two striking genetic traits. The first is an extraordinarily high frequency of the Y-chromosomal haplogroup R1b, reaching ~90% in Galicia (the highest in the Iberian Peninsula), 87% in the Basque Country, and exceeding 80% in Ireland and Brittany. The second is a dominant presence of the mitochondrial haplogroup H — a maternal lineage with deep European roots — that draws a continuous arc from Portugal to Belgium, peaking along the Cantabrian coast and Galicia at over 50%.

Haplogroup H, transmitted through the maternal line, suggests female demographic continuity reaching back to the Upper Palaeolithic or Mesolithic. Haplogroup R1b, transmitted through the paternal line, is conventionally associated with the migrations of steppe pastoralists who arrived in Western Europe during the Neolithic-Bronze Age transition. The combination of both — maximum paternal R1b, maximum maternal H — points to a pattern of male replacement over an autochthonous female substrate, a phenomenon documented across Western Europe during the third millennium BC.

But here a first problem arises. If R1b represents the steppe conquerors, and the steppe is the homeland of the Indo-European languages, then the peoples with the highest percentage of R1b should, in principle, be the most Indo-European. Are they?

To answer that question, we turned our gaze toward the most studied and most paradoxical case of all: the Basque.



II. The Basque Case Examined

II.1. The R1b Paradox

The Basque Country presents one of the highest R1b frequencies in all of Europe: between 83% and 87% depending on the study (Adams et al. 2008; Solé-Morata et al. 2017). The specifically Iberian subclade R1b-DF27 reaches 63–70% in the Basque Country, while the broader R1b-P312 (S116) haplogroup reaches 80% in some Basque provinces — 75% in Álava, 86.7% in Guipúzcoa, and 87.3% in Vizcaya (Adams et al. 2008). Only Galicia, with R1b approaching 90%, exceeds these figures in the Iberian Peninsula. Ireland, with comparable frequencies, completes the trio of western populations with extreme R1b.

However, the Basque Country is the home of the only surviving non-Indo-European language in Western Europe: Basque (Euskara). If the conventional equation $R1b = \text{Indo-European expansion}$ were correct, the Basques should speak an Indo-European language. They do not.

This paradox has been addressed in various ways in the literature. The dominant explanation for decades was that the Basques represented a Palaeolithic refuge, a pre-Indo-European population that had resisted Indo-Europeanization thanks to the geographic isolation of the western Pyrenees. Under this narrative, Basque would be a linguistic fossil, the last survivor of the languages spoken in Europe before the arrival of the Indo-Europeans.

This explanation, which we might call the “Basque paradigm,” has exerted a disproportionate influence on population genetics. For



years, the Basques were used as a reference to reconstruct the genetic profile of Palaeolithic Europe: it was assumed that, since their language was pre-Indo-European, their genetics must also be. But ancient genetics has demolished this presumption.

II.2. The Demolition of the Basque Paradigm

In 2019, a study by Olalde et al. published in *Science*, based on the genomic analysis of 271 ancient Iberian individuals, demonstrated that modern Basques are not genetically archaic. They are, in the study's own words, a "typical Iron Age population." Their autosomal profile — that is, their complete genome, not just the Y chromosome — is indistinguishable from that of other Iberian populations of the same period.

A subsequent study in 2021, based on the analysis of 1,900 Iberian genomes, further clarified: the genetic distinction of the Basques from their neighbours is due to "post-Iron Age genetic drift, not a divergent ancestral source." That is: the Basques are not different because they have preserved a Palaeolithic profile, but because they became isolated *after* the Iron Age, accumulating differences through drift in a gene pool that was originally indistinguishable from that of their neighbours.

The coup de grâce came from the Atapuerca data (2015): modern Basques are genetically more akin to Neolithic farmers than to Mesolithic hunter-gatherers. The "Palaeolithic people" turn out to be Neolithic.

Source	Finding	Implication
Olalde et al. 2019 (<i>Science</i>)	Basques = "typical Iron Age population"	Not a Palaeolithic refuge
1,900 genomes study 2021	Distinction due to "post-Iron Age drift"	Recent isolation, not ancestral divergence
Atapuerca 2015	Basques more akin to	The "Palaeolithic people" are Neolithic



Source	Finding	Implication
	Neolithic farmers than to hunter-gatherers	
Basque R1b: 83–87%	Second highest R1b in Spain	Maximum “steppe conquest” with non-IE language

The isolation hypothesis also fails on geographical grounds. If the Basques preserved their language thanks to Pyrenean isolation, how do we explain Gascony? The name Gascony derives from *Vasconia*. The Basques were present on both sides of the Pyrenees — including in the flat Garonne plain in southwestern France, where no geographic barrier could have protected them from Indo-European contact. If isolation explains Basque survival, Gascony disproves the isolation.

II.3. The Maternal Atlantic Arc: Haplogroup H

While the Y chromosome reveals steppe conquest, the maternal line tells a different story. Mitochondrial haplogroup H, the most frequent in Europe, is not distributed uniformly. Its highest frequency is recorded precisely along the Cantabrian coast and Galicia, where it exceeds 50%, and draws a continuous Atlantic arc descending from Belgium along the French coast to Portugal:

Region	H frequency (mtDNA)
Galicia / Cantabrian coast	~52%
Northern Portugal	~49%
Ireland	~47%
Brittany	~44%
Andalusia	~37–39%
Castilian meseta	~32%

The distribution of haplogroup H does not respect linguistic boundaries. The Basques, maternally, are indistinguishable from the Cantabrians, Asturians, or Galicians. There is no maternal genetic frontier at the Pyrenees. Basque “exceptionality” is exclusively



linguistic; genetically, they are part of the Atlantic continuum.

This datum is fundamental: the arc of maximum H coincides with the arc of maximum R1b. In Galicia both maxima converge: the highest paternal R1b and the highest maternal H in the entire Iberian Peninsula.

II.4. Varduli, Caristii, and Autrigones: The Celts of the Basque Country

If Basque is not Palaeolithic, how long has it been spoken in the present-day Basque Country? The answer from toponymy and epigraphy is unequivocal: not before the Early Middle Ages.

The peoples who inhabited the territory of the modern Basque Country during the Roman period were not Basque-speaking. The Varduli, Caristii, Autrigones, and Berones spoke Indo-European languages, probably Celtic or akin to Celtiberian. The evidence is overwhelming: of 75 documented toponyms in Caristii territory, 55 are of Indo-European etymology. There is not a single toponym with a secure Basque root (-berri, -egi, Iltur-) in the oldest record of these territories. These tribes were, according to Almagro Gorbea (2014b), “peoples of Celtic-Atlantic culture, language, and ethnicity, like all the populations of the Cantabrian region.”

The idea of a late Basquization — after the fall of the Roman Empire — is now the consensus among specialists. Caro Baroja, Mitxelena, and Sánchez Albornoz had already formulated it in the twentieth century. The Chronicle of Alfonso III (9th century) states it with meridian clarity: “*Bardulia quae nunc appellatur Castella*” — Bardulia, which is now called Castile.

Where did Basque come from? From the Pyrenean strip, where it was documented since the Roman period: Aquitania to the north, Navarra to the south. Aquitanian — recorded in some 400 anthroponymic inscriptions and around 70 theonymic ones in the



Haute-Garonne (1st–3rd centuries AD) — is recognized as the ancient form of Basque. But it is Aquitania, not Vizcaya.

Furthermore, Basque was not a single language. The dialectal diversity of Basque was so extreme that, as the 18th-century author Joannes d’Etcheverry observed, “a Low Navarrese or one from Zuberoa could not understand a Vizcayan.” Georges Lacombe divided the Basque dialects into “Vizcayan and the rest.” The unified Basque (*euskara batua*) was created only in 1968 at the Congress of Arantzazu. Before then, what existed was not a language but several mutually unintelligible speech forms. This internal diversity, far from supporting antiquity, is more consistent with a recent expansion across linguistically diverse terrain.

II.5. The Portuguese Evidence: Martiniano et al. 2017

The most detailed genomic study of the Atlantic Neolithic-to-Bronze Age transition in Iberia comes from Martiniano et al. (2017), published in *PLoS Genetics*. This study, conducted by Trinity College Dublin with the University of Coimbra, analyzed 14 ancient Portuguese individuals spanning the Middle Neolithic (4200–3500 BC) to the Middle Bronze Age (1740–1430 BC).

The Y-chromosome data from these 14 individuals tell a stark story:

Sample	Site	Period	Sex	Y-chromosome	mtDNA
LC41	Lugar do Canto	Middle Neolithic	XX	—	U5b1
LC42	Lugar do Canto	Middle Neolithic	XX	—	H3
LC44	Lugar do Canto	Middle Neolithic	XX	—	H1e1a2
LC45	Lugar do Canto	Middle Neolithic	XY	—	—
CA117B	Cabeço da	Late Neol./Chalcol	XY	I2a1b	J1c1b



Sample	Site	Period	Sex	Y-chromosome	mtDNA
	Arruda	ithic			
CA122A	Cabeço da Arruda	Late Neol./Chalcolithic	XY	G2a2a1	H1e1a
CM364	Cova da Moura	Late Neol./Chalcolithic	XY	I2a1b	H
CM9B	Cova da Moura	Late Neol./Chalcolithic	XX	—	J1c1
DA96B	Dolmen de Ansião	Late Neol./Chalcolithic	XY	I2a1a1a1b	K1b1a
MC337A	Monte Canelas	Late Neol./Chalcolithic	XY	—	—
MG104	Monte do Gato	Middle Bronze Age	XY	R1b1a2a1a2	U5b3
TV32032	Torre Velha 3	Middle Bronze Age	XY	R1b1a2	X2b
TV3831	Torre Velha 3	Middle Bronze Age	XY	R1b1a2a1a2	H1
VO10207	Monte do Vale do Ouro	Middle Bronze Age	XX	—	U5b1

The pattern is absolute. The Neolithic and Chalcolithic males carry I2 (Western Hunter-Gatherer lineage) and G2a (Anatolian farmer lineage). The Bronze Age males — all three of them — carry R1b. One hundred percent Y-chromosome turnover.

Yet Martiniano describes the overall genetic influx as “subtle” and “comparatively modest” compared to Northern Europe. How? Because the autosomal DNA (the complete genome, not just the Y chromosome) shows that the Portuguese Bronze Age individuals



cluster closer to the Atlantic Neolithic populations than to Central European ones. A few incoming males achieved reproductive dominance — whether through elite status, polygyny, or some other mechanism — without completely replacing the existing population's autosomal genome.

The study also identified an “Atlantic_Neolithic” genetic cluster that groups the Portuguese Middle and Late Neolithic individuals with Irish (Ballynahatty, ~3343–3020 BC) and Scandinavian (Gökhem 2, southwestern Sweden, ~3050–2750 BC) Neolithic farmers. This Atlantic genetic identity — shared across 2,000 km of coastline from Portugal to Sweden — existed between approximately 4200 and 2500 BC. It breaks apart in the Bronze Age: the Portuguese Bronze Age individuals form their own cluster, shifted toward Central European patterns but still closer to the Atlantic Neolithic than to the steppe.

Critically, this study has no samples from Galicia. Not one. The Atlantic northwest remains a genomic black hole.

II.6. Section Summary

The Basque paradox dissolves when the terms are reformulated. The Basques are not an exception to the steppe model: they have the second highest R1b in Spain, a maternal haplogroup H indistinguishable from that of their Atlantic neighbours, and an autosomal profile of Iron Age origin, not Palaeolithic. Their language is not a Palaeolithic fossil but a Pyrenean tongue that expanded late over a Celtic substrate. The “Basque paradigm” has been disproven by genetics, toponymy, and epigraphy.

But the underlying question remains: why does a population with 87% R1b speak a non-Indo-European language? If R1b marks the arrival of the Indo-Europeans, how did the Basques escape the linguistic shift that accompanied the genetic shift?



To address this question, we need to broaden our gaze. The Basque case is not unique.

III. Non-Indo-European ≠ Pre-Indo-European

III.1. The Foundational Logical Error

Classical Indo-European studies were built upon an axiom that is rarely examined: if a language is non-Indo-European, then it is *pre-Indo-European*. That is, it predates the arrival of the Indo-Europeans. This axiom was logical so long as it was assumed that the Indo-Europeans had arrived in Europe at a relatively recent date, replacing a linguistically homogeneous population already there.

But the axiom contains an elementary logical error. “Non-Indo-European” does not imply “prior to Indo-European.” It implies only “different from Indo-European.” A non-Indo-European language may be contemporary with, later than, or earlier than Indo-European. The temporal relationship is not deducible from the typological relationship.

This error has had profound historiographical consequences. Theo Vennemann (1994, 2003) constructed an elaborate hypothesis of “Europa Vasconica” in which a proto-Basque substrate underlay the entire European hydronymy — the so-called “Old European” river names. His reasoning was impeccable within the traditional framework: if in the Palaeolithic there was a vast pre-Indo-



European substrate in Europe, and Basque was a relic of that substrate, and the ancient hydronymy represented an ancient layer, then the hydronymy must be proto-Basque. But Joseba Lakarra (1996) demolished this hypothesis on purely phonological grounds: the reconstructed proto-Basque lacked initial /r/, had almost no final /a/, had no muta cum liquida clusters, and no /nt/ group — all features abundantly present in the Palaeolithic European hydronymy. The phonologies are simply incompatible.

Vennemann's failure is instructive because it shows what happens when the axiom "non-IE = pre-IE" is taken to its logical conclusion. If the axiom is wrong, the entire edifice collapses.

III.2. The Etruscans: The Paradox Repeated

In 2021, Posth et al. published in *Science Advances* a genomic study of 82 Etruscan individuals spanning nearly two millennia (800 BC – AD 1000). The results were extraordinary:

75% of Etruscan males belonged to haplogroup R1b (R1b-M269, especially R1b-P312 and its derivative R1b-L2/U152).

The most common mitochondrial haplogroup was H.

No recent admixture with Anatolian or Eastern Mediterranean populations was detected.

The Etruscans were genetically **indistinguishable from the contemporary Latins** living in neighbouring Rome.

The Etruscan genetic profile remained stable for nearly 800 years, from the post-Villanovan period to the end of the Roman Republic. In the researchers' own words: "this linguistic persistence, combined with a genetic turnover, challenges simple assumptions that genes equal languages." The researchers further noted that "considering that steppe-related groups were likely responsible for the spread of Indo-European languages, now spoken around the



world by billions of people, the persistence of a non-Indo-European Etruscan language is an intriguing and still unexplained phenomenon.”

Johannes Krause, co-director of the Max Planck Institute for Evolutionary Anthropology, was more explicit: “It is likely that the Etruscan language — as well as Basque, Paleo-Sardinian, and Minoan — developed on the continent in the course of the Neolithic Revolution” (Krause 2021).

The Etruscan language belongs to the Tyrsenian family, which also includes Rhaetic (once spoken in the Alps) and Lemnian (from the island of Lemnos in the Aegean). The Alpine location of Rhaetic is significant: it places the Tyrsenian family in exactly the Central European zone from which the Urnfield culture originated.

Trait	Basques	Etruscans
Language	Non-Indo-European (Basque)	Non-Indo-European (Etruscan)
Paternal R1b	83–87%	75%
Predominant mtDNA	H	H
Genetically distinct from IE neighbours	No (Olalde 2019)	No (Posth 2021)
Cultural affiliation	Urnfield (via Aquitania)	Urnfield (Villanovan)
Steppe ancestry	Yes (high)	Yes (high)

The parallel is exact. Two peoples speaking non-Indo-European languages, with massive steppe genetics (R1b + H), situated at opposite ends of the western Mediterranean, both genetically indistinguishable from their neighbours who do speak Indo-European languages. And both linked to the Urnfield culture.

The difference in R1b percentages between Etruscans (75%) and modern Basques (87%) may simply reflect the 200-year gap between the Etruscan samples (900–600 BC) and the modern



Basque samples. If Iron Age Basques were sampled at the same date as the Etruscans, they might well show a similar 75% frequency.

III.3. The Urnfield Culture and the Non-Indo-European Peoples

The Villanovan culture, the earliest phase of Etruscan civilization (ca. 900 BC), derives directly from the Proto-Villanovan culture, which is in turn an offshoot of the Central European Urnfield (*Urnenfelder*) cultural system, dated to around 1200 BC. This is not speculation; it is the current archaeological consensus.

Xaverio Ballester, in an article published in *Palaeohispanica* (2018), argued that three historical non-Indo-European languages can be confidently linked to expansions of the Urnfield culture:

People	Language	Culture
Iberians	Non-Indo-European	Urnfield
Aquitanians (proto-Basques)	Non-Indo-European	Urnfield
Etruscans	Non-Indo-European	Urnfield

If these three peoples are linked to the Urnfield — a Central European Late Bronze Age phenomenon — then they cannot be “pre-Indo-European.” They are Bronze Age peoples, contemporary with Indo-European cultures. If they are pre-Indo-European, then Indo-European is just as “pre-” as they are. The terminology becomes absurd. Nobody is “pre-” anybody. They are contemporaries competing for territory in the first millennium BC.

Ballester’s argument rests on the work of several authorities. Almagro Gorbea (2005, 2008, 2014) provides the archaeological and onomastic framework for the Celtic substrate in the Basque Country. Francisco Villar (2005, 2011) supplies the linguistic analysis of the Indo-European presence in Iberia. Joseba Lakarra (1996) furnishes the phonological demolition of the Vennemann



hypothesis. And Miquel Tarradell (1962) supplies the archaeological model for the two Urnfield waves into Iberia.

IV. The Urnfield Conglomerate

IV.1. Two Infiltrations, Two Peoples

The relationship between the Urnfield culture and the Iberian Peninsula was precisely described by the Catalan archaeologist Miquel Tarradell in his work *Les arrels de Catalunya* (1962). Tarradell identified two distinct migratory waves.

The **first wave** (8th century BC, possibly earlier) originated from the Rhine basin and the Upper Rhône. It entered through Roussillon and settled in the regions of Vallès, Penedès, Camp de Tarragona, and Urgell. These were agricultural people who did not significantly cross the Ebro. According to Tarradell, "this group, within the whole of the Urnfield culture, is a rather ancient group, which must have arrived... in the 8th century and perhaps even a little before, corresponding to the periods that Central European prehistorians call Hallstatt B and C." Furthermore, "the new civilization, imposing itself on all of Catalonia, erased many characteristics of the preceding centuries... one cannot doubt the change manifested in religion... and in material culture."

The **second wave**, shortly after, was denser and more complex. It entered through multiple Pyrenean passes, especially via the Cerdanya and the Segre valley. It originated from northwestern



Italy and southern Switzerland. Unlike the first, these were pastoral people who tended to settle in mountainous terrain. They intensely occupied the Ebro valley. As Tarradell wrote, they “came from northwestern Italy and the southern part of Switzerland.”

Wave	Origin	Route	Settlement	Economy	Identification (Ballester)
First (8th c. BC)	Rhine / Upper Rhône	Roussil lon	Catalonia (plains)	Agricultu ral	Iberians
Secon d (8th– 7th c. BC)	NW Italy / S. Switzerl and	Multipl e Pyrene an passes	Pyrenees / Ebro valley	Pastoral	Aquitanians / proto-Basques

What Tarradell described as two waves of Indo-European invaders, Ballester proposes to invert: where Tarradell says “Indo-European,” one should read “non-Indo-European,” and vice versa. As Tarradell himself wisely cautioned: “it often happens that linguists make use of data from archaeologists, which they give as certain when they are far from it. And we often find that archaeologists want to help hypotheses with linguistic information that at a given moment seems solid and then falls apart... one has the impression that both live inside a vicious circle.”

Ballester’s inversion breaks the vicious circle. And it is backed by a specific archaeological argument: there is a detectable Indo-European substrate in the toponymy of lands that would later be historically documented as Iberian, indicating that the Iberians displaced a prior Indo-European population.

IV.2. The Ora Maritima Evidence

The *Ora Maritima* of Avienus, whose principal sources date back to Greek authors of the 6th century BC (Schulten 1922), describes a territory south of the Ebro where the toponymy is clearly Indo-



European: Berybraces, Crabassiæ, Hylactes, Hystra, Lebedontia, Sarna (cf. the Celtiberian SARNICi). However, in the documentation of the Roman period, that same territory shows Iberian toponymy: Biskargís, ILDVM, ILERCAVONIA, Intibili, SEBELACI.

The conclusion is inescapable: there were no Iberians — or not significantly — south of the Ebro in the 6th century BC. The Iberian presence in the region is later, and replaces a prior Indo-European substrate.

IV.3. Iberian as a Graphic Illusion

If the Iberians were a recently arrived people, why does their language appear so homogeneous? Javier Velaza (2006), one of the leading specialists in Palaeohispanic languages, noted this apparent contradiction: “from the earliest texts, the Iberian language seems very homogeneous... it is incredible that it would not have undergone a much more marked process of dialectalization... that a language like Iberian should remain so homogeneous for so long, not being linked to a centralizing political power, would constitute a surprising phenomenon.”

The solution may lie in the nature of “Iberian” as a documented language. The Iberian script was used to write both Iberian and Celtiberian — two completely different languages, one non-Indo-European and one Indo-European. If the same writing system served for entirely unrelated languages, it could a fortiori mask differences within related ones.

Noemí Moncunill, of the University of Barcelona, put it clearly: “we should consider that in antiquity there was a language, let us say Basque-like, that constituted a continuum with multiple different speech forms.” What we call “Iberian” may not be a single language but a koiné, a commercial lingua franca used by peoples of diverse speech. The writing unifies what the ear would separate.



IV.4. The Iberian-Basque Connection

The relationship between Iberian and Basque has been debated since the 19th century. The strongest modern case for a connection comes from Eduardo Orduña Aznar, who demonstrated that the Iberian numerals correspond to Basque numerals, that both languages share ergativity and the genitive morpheme *-en*, and that the Iberian verb *egiar/ekiar* corresponds to the Basque *egin* (to do/make). Even Jürgen Untermann, the foremost authority on Palaeohispanic languages, who had long opposed the Iberian-Basque connection, converted to the vasco-iberist position before his death. The current consensus is not that Iberian *is* Basque, but that they belong to the same language family.

IV.5. The Ligurians and the Western Frontier

The Ligurians, whose original extent was far greater than modern Liguria — from Catalonia to the Arno (Pisa), including the Rhône valley — were pushed eastward by the Iberians in the 7th century BC. The majority consensus among specialists (de Bernardo Stempel, Delamarre, Untermann, de Hoz, Rubat Borel, Mees) is that Ligurian was an Indo-European language, probably an archaic Celtic dialect or an IE language related to Celtic. The map of first-millennium BC Western Europe thus shows non-Indo-European Urnfield peoples (Iberians, Aquitanians, Etruscans) entering already Indo-European territories (Celts, Ligurians, Lepontii) and displacing or superimposing themselves upon them.



V. The Eastern Connection

V.1. Ballester's 23 Isoglosses

If Iberians, Aquitanians, and Etruscans are not pre-Indo-European but peoples of Central European origin linked to the Urnfield, with which languages are they related? Ballester has identified 23 potential isoglosses shared between the Hispano-non-Indo-European group (Iberian and Basque) and the Turkic and Uralic groups — but *not* shared by the Indo-European group. These include: oxytony (possible in Iberian and Basque, present in Turkic), vowel harmony (possible in both, present in Turkic and Uralic), rarity of initial /d/ (present in all three non-IE groups), absence of /p/ (present in all three), no initial /r-/ (present in all four groups), agglutination (present in all four), no grammatical gender (present in Basque, Turkic, and Uralic), and preverbal focalization (present in Basque and Turkic).

These phonological, morphological, and syntactic affinities are more consistent with a Central/Western Asian provenance than with a European Palaeolithic survival.

V.2. The Basque-Caucasian Hypothesis Revisited

The idea of a relationship between Basque and North Caucasian languages is not new. Bengtson, Uhlenbeck, Dumézil, and Lafon have at various times proposed a Basque-Caucasian family linking Basque with the Nakh-Daghestanian languages (Chechen, Avar, Lak, Dargi). The shared vocabulary includes agricultural and pastoral terms, suggesting a contact or kinship dating to the Neolithic or Chalcolithic, not the Palaeolithic.



If proto-Basque travelled with R1b carriers from the North Caucasus toward Western Europe, it would not be a “pre-Indo-European” language but a language *contemporary* with Proto-Indo-European that took a different route. Not earlier, but parallel.

V.3. The Overwritten Caucasus and the Periphery/Corridor Principle

Current genetic data from the North Caucasus show a range of R1b from 0% (in peoples with dominant J1, such as the Hunzib) to 68% (in the Bagvalins). The J1 and J2 haplogroups, associated with Fertile Crescent expansions, have rewritten the Caucasian genetic profile.

From this a general principle emerges: **peripheries preserve; corridors destroy**. A geographic finisterre like Galicia, Brittany, or Ireland — a dead end where nobody comes afterwards to dilute the gene pool — preserves signals that a corridor like the Caucasus, traversed by wave after wave of migrations, erases.

If R1b was born in or transited through the Caucasus 6,000 years ago, we would not expect to find its reliable record there, but rather in the Atlantic finisterre, where no one has come afterward to overwrite it. And it is in the Atlantic finisterre that we find the highest R1b frequencies on the planet.



VI. The Ghost of L51

VI.1. Two Brothers, Two Destinies

Haplogroup R1b-M269 subdivides into two main branches under R1b-L23:

R1b-Z2103: the eastern branch. Found in all Yamnaya samples analyzed to date.

R1b-L51: the western branch. Ancestor of P312 (and of its Iberian derivative DF27), of U106, and of all the subclades that dominate Western Europe today.

L51 and Z2103 are siblings. Both descend from L23, whose common ancestor is estimated at around 3800 BC (FTDNA Discover; YFull). They separated *before* the Yamnaya expansion.

R1b-L23 (~3800 BC)

├ Z2103 → Pontic steppe → Yamnaya → Afanasevo → Mongolia
└ L51 → ??????? → Bohemia 2900 BC → Bell Beaker → ALL of Western Europe

VI.2. Z2103 in the Steppe: A Complete Record

Date (BC)	Location	R1b subclade	Culture
~4800–4500	Volga (Khvalynsk)	R1b (+ V1636)	Khvalynsk
~3400	N. Caucasus (Sharakhalsun)	Z2103	Maikop
~3300–2600	Southern steppe (Samara, Don, Volga)	Z2103 (ALL samples)	Yamnaya
~3300–2500	Altai, western Mongolia	Z2103	Afanasevo
~3100	Lopatino, Samara	L23 (Y410+, L51 negative)	Yamnaya



Date (BC)	Location	R1b subclade	Culture
	(I0443)		
~2800–2200	Western steppe	Z2103	Catacomb
~2700–2100	Middle Volga	Z2103	Poltavka
~2100–1800	Southern Urals	Z2103 + R1a-Z93	Sintashta

The Lopatino sample (I0443) is particularly significant: it is L23-positive but L51-negative. The father (L23) has been found in the steppe. The eastern son (Z2103) in abundance. But the western son (L51) — never.

VI.3. L51: The Ghost

R1b-L51 has never been found in the Pontic steppe. Not in Yamnaya. Not in Afanasevo. Not in Catacomb. Not in Poltavka. Not in Sintashta. Not in any site sampled to date.

The first documented appearance of L51 is in **Bohemia** (Czech Republic), in a Corded Ware context, around **2900 BC** (Papac et al. 2021). The earliest samples of L151 (a subclade of L51) appear in this same Bohemian context, with autosomal DNA of “steppe type” but a Y chromosome without documented precedent in the steppe.

Razib Khan, the population geneticist, noted in his Substack: “The first thing to note is that the Yamnaya samples were R1b, but of a haplogroup distinctive from that of the R1b common in Western Europe, and brought by the Bell Beakers.” And: “the division between Yamnaya R1b and Bell Beaker R1b dates to 4000 BC.”

Where was L51 between 3800 BC (its estimated birth) and 2900 BC (its first appearance in Bohemia)? The conventional answer is: “it must have been somewhere in the western steppe or the Carpathian Basin, but we haven’t found it yet.” But the Yamnaya have been intensively sampled over the last decade — dozens of individuals from multiple sites, from the Don to the Urals — and in



none of them has L51 appeared.

VI.4. The Black Hole of the Atlantic Bronze Age

The documented chronology of L51 and its derivatives:

Date (BC)	Location	Subclade	Culture
~2900	Bohemia (Czech Rep.)	L151 (xU106, xP312)	Corded Ware
~2900	Bohemia	U106	Corded Ware
~2600–2500	Germany (Kromsdorf)	M269	Bell Beaker
~2460–2300	France (Grotte Basse)	DF27>Z195	Bell Beaker
~2460–2200	Germany (Bavaria, Lech)	DF27	Bell Beaker
~2460–2200	England (Boscombe Down)	P310/L151*	Bell Beaker
~2500–2000	Northern Spain	M269	Iberian Bell Beaker
~1740–1430	Portugal (Martiniano)	R1b (3/3 males)	Bronze Age

The apparent direction is east to west. But there is a colossal void in this sequence.

There is no ancient DNA sample from the European Atlantic seaboard (Galicia, Brittany, Ireland, Atlantic Portugal) between 3000 and 2000 BC.

R1b-DF27, the specifically Iberian subclade that today dominates the peninsula (40–70% depending on region), has an estimated molecular clock age of ~4,200 years (ca. 2200 BC), with its greatest diversity in Aragon and the Iberian northeast (Solé-Morata et al. 2017). But the first physical sample of DF27 is from France, dated around 2380 BC. Between the molecular birth of DF27



(~3000 BC according to YFull) and its first physical appearance (2380 BC), there is a 600-year void.

R1b-DF27 frequency distribution across Iberia reveals a notable pattern: the highest frequencies of undifferentiated DF27* (that is, DF27 chromosomes not belonging to any known subclade) are found precisely in the Atlantic west — Galicia (57%), Asturias (43%), and Portugal — regions that “may harbour yet unknown branches of R1b-DF27” (Solé-Morata et al. 2017). These unknown western branches could represent the oldest, most basal lineages of DF27 — or they could be something else entirely that only Atlantic Bronze Age ancient DNA could resolve.

VII. The Final Question

VII.1. The Direction of Travel as Assumption

The entire conventional narrative of European population genetics assumes a direction: east to west. R1b is born in the steppe, travels with the Yamnaya pastoralists, transforms into Bell Beaker upon passing through Central Europe, and arrives at the Atlantic as the final wave of a 2,000-year expansion.

But this direction is not a datum. It is an assumption. The empirical data state the following:

Z2103 (the eastern branch of R1b-L23) is abundantly documented in the steppe from 3300 BC.



L51 (the western branch of R1b-L23) **has never been found** in the steppe.

L51 first appears in Bohemia around 2900 BC, already with autosomal DNA of steppe type but with a Y chromosome without documented precedent in the steppe.

L51 expands westward with the Bell Beaker during the following centuries.

The Atlantic finisterre — the supposed point of arrival — has not been sampled for the relevant period (3000–2000 BC).

The modern populations of the Atlantic finisterre present the highest R1b frequencies on the planet (Galicia ~90%, Ireland >80%, Basque Country 87%).

If we only have data from the presumed point of departure (the steppe) and the midpoint (Central Europe), but not from the point of arrival (the Atlantic), the direction of travel is indeterminate.

VII.2. The Alternative Hypothesis

We do not claim that Atlantic R1b is autochthonous. We do not have the data to claim this. But neither is there data to deny it, and this absence of data is, in itself, a finding that deserves attention.

Consider the possibility: what if L51 did not travel from east to west? What if the bifurcation of L23 into Z2103 and L51 (~3800 BC) did not occur in the steppe but elsewhere — perhaps in the Carpathian Basin, perhaps farther west — and each sibling took a different direction? Z2103 toward the east, where we find it abundantly. L51 toward the west, where it dominates today but where no one has looked for the third millennium.

Or consider an even more radical possibility: what if L51 was already in Western Europe, and the “steppe” ancestry detected in the earliest L51 carriers in Bohemia reflects a bidirectional mixture



— not only the east flowing west, but also the west interacting with the east?

VII.3. The Burial Bias Hypothesis

There is a further consideration that complicates the interpretation of all Bronze Age genetic data from Atlantic Europe. If the Atlantic Bronze Age peoples deposited their dead in water — in rivers, estuaries, bogs, and the sea — as the archaeological evidence of riverine deposits suggests (Ruiz-Gálvez Priego 1995), then the individuals who *are* found in earth burials may not be representative of the population as a whole. They may represent precisely the incoming R1b-bearing elite who brought a different funerary custom — earth burial — from outside the Atlantic tradition. In this scenario, the three Portuguese Bronze Age males of Martiniano who are all R1b are not evidence that the entire population was R1b; they are evidence that the people who buried in earth were R1b. The I2 and G2a lineages did not necessarily disappear; they simply stopped being visible to archaeologists because their bearers continued the Atlantic tradition of water deposition.

This hypothesis — which we might call the burial bias hypothesis — cannot be confirmed or refuted with current data. But it explains, more economically than a phantom genocide, why 100% Y-chromosome replacement appears in the burial record without any archaeological trace of violence.

VII.4. The Finisterre as Laboratory

The principle we have stated — peripheries preserve, corridors destroy — has a direct methodological implication. If we want to know what was in Western Europe during the third millennium BC, we must look where no one has looked: in Galicia, in Brittany, in Ireland, on the Atlantic coast of Portugal.



The day the first genomic sequence from an Atlantic Bronze Age individual — from the third millennium BC — from Galicia, Brittany, or Ireland is published, we will know whether L51 arrived from the east or was already there. Until then, the direction of travel of western R1b is an open question.

And the question about the makers of the Mogor labyrinths, which was the origin of this investigation, remains unanswered. We only know that whoever carved them lived in a finisterre that ancient genetics has not yet explored.

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